REMARKS

In the Notice of Non-Compliant Amendment mailed June 14, 2001, the Office requested submission of an amendment in compliance with 37 C.F.R. § 1.121. Previously, in a Notice to Comply (Paper No. 9) mailed April 17, 2001, the Examiner requested that the claims, specification and drawings be amended to identify sequences by their SEQ ID NO. Accordingly, Applicants have submitted this amendment in response to both Notices, and have amended the application to provide the information requested by the Examiner. No new matter enters by this amendment.

Particularly, the references to Figures 1, 21, and 22 on pages 4 and 34-35 have been amended by adding SEQ ID NOs that correspond with the listed sequences. Support for these amendments may be found in the original claims, the specification, the sequence listing, and the Figures, *e.g.*, at page 22, line 25 through page 23, line 4; page 24, lines 3-6; page 30, lines 5-14; page 34, line 7 through page 36; and in Figures 1, 21, and 22. The references to Figures 2 through 20 on pages 28-29 have also been amended by adding SEQ ID NOs that correspond with the listed sequences. Support for these amendments may be found in the original claims, the specification, the sequence listing, and the Figures, *e.g.*, at page 28, lines 6-11, page 29, lines 1-3, and in Figures 2 through 20. No new matter enters by these amendments.

Claims 5-10 have been cancelled, claims 13-19 have been amended, and claims 34-41 have been added. The application presently includes claims 1-4 and 11-41. Claims 13-19 have been amended to correct minor typographical errors. Support for new claims 34-41 is found throughout the original claims, the specification, the sequence listing, and the Figures, *e.g.*, at page 22, line 25 through page 23, line 4; page 24, lines 3-6; page 28, line 6 through page 29, line

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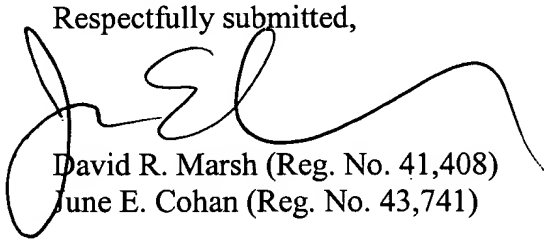
19; page 30, lines 5-14; page 34 line 7 through page 36; and in Figures 1-3, 9, 21, and 22. No new matter enters by these amendments.

The presently pending claims are believed to be in immediate condition for allowance. Accordingly, the Examiner is respectfully requested to pass this application to issue. The Examiner is respectfully requested to contact Applicants' undersigned representative at 202.942.5071 to address any unresolved issues remaining in this application.

The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to our Deposit Account No. 50-1824 referencing charge number 16516.105.

Respectfully submitted,



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Marked-Up Claims

13. (Amended) A nucleic acid construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding **a** prenyltransferase, and a transcriptional termination region.

14. (Amended) A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding **a** prenyltransferase is obtained from an organism selected from the group consisting of a eukaryotic organism and a prokaryotic organism.

15. (Amended) A nucleic acid construct according to Claim 14, wherein said nucleic acid sequence encoding **a** prenyltransferase is obtained from a plant source.

16. (Amended) A nucleic acid construct according to Claim 15, wherein said nucleic acid sequence encoding **a** prenyltransferase is obtained from a source selected from the group consisting of *Arabidopsis,* soybean and corn.

17. (Amended) A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding **a** prenyltransferase is obtained from *Synechocystis.*

18. (Amended) A plant cell comprising the construct of [Claim13] **Claim 13**.

19. (Amended) A method for the alteration of the tocopherol content in a host cell, comprising[;] transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding **a** prenyltransferase, and a transcriptional termination region.

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Marked-Up Specification

On page 4, lines 3-4, the following changes have been made:

Figure 1 provides an amino acid sequence alignment between ATPT2, ATPT3, ATPT4, ATPT8, and ATPT12 **(SEQ ID NOs: 2, 4, 6, 12 and 17, respectively),** [are] performed using ClustalW.

On page 4, lines 24-28, the following changes have been made:

Figure 21 provides an amino acid sequence alignment using ClustalW between the *Synechocystis* sequence knockouts **slr1736, slr0926, sll1899, slr0056, and slr1518 (SEQ ID NOs: 37, 32, 33, 34 and 35, respectively)**.

Figure 22 provides an amino acid sequence of the ATPT2, ATPT3, ATPT4, ATPT8 and ATPT12 protein sequences from *Arabidopsis* **(SEQ ID NOs: 2, 4, 6, 12 and 17, respectively)** and the slr736, slr0926, sll1899, slr0056, and the slr1518 amino acid sequences from *Synechocystis* **(SEQ ID NOs: 37, 32, 33, 34 and 35, respectively)**.

On page 28, line 6 through page 29, line 19, the following changes have been made:

The sequence encoding ATPT2 prenyltransferase **(SEQ ID NO: 1)** was cloned in the sense orientation into pCGN8640 to produce the plant transformation construct pCGN10800 (Figure 2). The ATPT2 sequence is under control of the 35S promoter.

The ATPT2 sequence **(SEQ ID NO: 1)** was also cloned in the antisense orientation into the construct pCGN8641 to create pCGN10801 (Figure 3). This construct provides for the antisense expression of the ATPT2 sequence from the napin promoter.

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The ATPT2 coding sequence **(SEQ ID NO: 1)** was also cloned in the antisense orientation into the vector pCGN8643 to create the plant transformation construct pCGN10802.

The ATPT2 coding sequence **(SEQ ID NO: 1)** was also cloned in the antisense orientation into the vector pCGN8644 to create the plant transformation construct pCGN10803 (Figure 4).

The ATPT4 coding sequence **(SEQ ID NO: 5)** was cloned into the vector pCGN864 to create the plant transformation construct pCGN10806 (Figure 5).

The ATPT2 coding sequence **(SEQ ID NO: 1)** was cloned into the vector pCGN864 to create the plant transformation construct pCGN10807 (Figure 6).

The ATPT3 coding sequence **(SEQ ID NO: 3)** was cloned into the vector pCGN864 to create the plant transformation construct pCGN10808 (Figure 7). The ATPT3 coding sequence **(SEQ ID NO: 3)** was cloned in the sense orientation into the vector pCGN8640 to create the plant transformation construct pCGN10809 (Figure 8). The ATPT3 coding sequence **(SEQ ID NO: 3)** was cloned in the antisense orientation into the vector pCGN8641 to create the plant transformation construct pCGN10810 (Figure 9). The ATPT3 coding sequence **(SEQ ID NO: 3)** was cloned into the vector pCGN8643 to create the plant transformation construct pCGN10811 (Figure 10). The ATPT3 coding sequence **(SEQ ID NO: 3)** was cloned into the vector pCGN8640 to create the plant transformation construct pCGN10812 (Figure 11).

The ATPT4 coding sequence **(SEQ ID NO: 5)** was cloned into the vector pCGN8640 to create the plant transformation construct pCGN10813 (Figure 12). The ATPT4 coding sequence **(SEQ ID NO: 5)** was cloned into the vector pCGN8643 to create the plant transformation construct pCGN10814 (Figure 13). The ATPT4 coding sequence **(SEQ ID NO: 5)** was cloned into the vector pCGN8641 to create the plant transformation construct pCGN10815 (Figure 14).

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The ATPT4 coding sequence **(SEQ ID NO: 5)** was cloned in the antisense orientation into the vector pCGN8644 to create the plant transformation construct pCGN10816 (Figure 15).

The ATPT2 coding sequence **(SEQ ID NO: 1)** was cloned into the vector pCGN???? to create the plant transformation construct pCGN10817 (Figure 16). The ATPT8 coding sequence **(SEQ ID NO: 11)** was cloned in the sense orientation into the vector pCGN8643 to create the plant transformation construct pCGN10819 (Figure 17).

The ATPT12 coding sequence **(SEQ ID NO: 16)** was cloned into the vector pCGN8644 to create the plant transformation construct pCGN10824 (Figure 18). The ATPT12 coding sequence **(SEQ ID NO: 16)** was cloned into the vector pCGN8641 to create the plant transformation construct pCGN10825 (Figure 19). The ATPT8 coding sequence **(SEQ ID NO: 11)** was cloned into the vector pCGN8644 to create the plant transformation construct pCGN10826 (Figure 20).

On page 34, lines 7-9, the following changes have been made:

The amino acid sequences for the *Synechocystis* knockouts **slr1736, slr0926, sll1899, slr0056 and slr1518 (SEQ ID NOs: 37, 32, 33, 34 and 35, respectively)** are compared using ClustalW, and are provided in Table 3 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 21.

On page 34, line 11 through page 35, line 2, the following changes have been made:

Amino acid sequence comparisons are performed using various *Arabidopsis* prenyltransferase sequences **(ATPT2 (SEQ ID NO: 2), ATPT3 (SEQ ID NO: 4), ATPT4 (SEQ ID NO: 6), ATPT8 (SEQ ID NO: 12) and ATPT12 (SEQ ID NO: 17))** and the *Synechocystis* sequences **(slr1736 (SEQ ID NO: 37), slr0926 (SEQ ID NO: 32), sll1899 (SEQ**

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ID NO:33), slr0056 (SEQ ID NO:34), and slr1518 (SEQ ID NO: 35)). The comparisons are presented in Table 4 below. Provided are the percent identities, percent similarity, and the percent gap. The alignment of the sequences is provided in Figure 22.

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